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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=8; day=26; hr=16; min=0; sec=22; ms=969;]

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Application No: 10595585

Version No: 1.0

Input Set:

Output Set:

Started: 2008-07-22 21:11:18.188

Finished: 2008-07-22 21:11:19.445

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 257 ms

Total Warnings: 21

Total Errors: 0

No. of SeqIDs Defined: 21

Actual SeqID Count: 21

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

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Actual SeqID Count: 21

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

<110> YANG, Beom-Seok
PARK, Sung-Dae

<120> DDR2 PROTEIN WITH ACTIVATED KINASE ACTIVITY
AND PREPARATION METHOD THEREOF

<130> 300602005700

<140> 10595585

<141> 2008-07-22

<150> PCT/KR2004/002784

<151> 2004-11-01

<150> KR10-2003-0076967

<151> 2003-10-31

<160> 21

<170> KopatentIn 1.71

<210> 1

<211> 855

<212> PRT

<213> Artificial Sequence

<220>

<223> Human DDR2 protein synthetic construct

<400> 1

Met Ile Leu Ile Pro Arg Met Leu Leu Val Leu Phe Leu Leu Leu Pro
1 5 10 15

Ile Leu Ser Ser Ala Lys Ala Gln Val Asn Pro Ala Ile Cys Arg Tyr
20 25 30

Pro Leu Gly Met Ser Gly Gly Gln Ile Pro Asp Glu Asp Ile Thr Ala
35 40 45

Ser Ser Gln Trp Ser Glu Ser Thr Ala Ala Lys Tyr Gly Arg Leu Asp
50 55 60

Ser Glu Glu Gly Asp Gly Ala Trp Cys Pro Glu Ile Pro Val Glu Pro
65 70 75 80

Asp Asp Leu Lys Glu Phe Leu Gln Ile Asp Leu His Thr Leu His Phe
85 90 95

Ile Thr Leu Val Gly Thr Gln Gly Arg His Ala Gly Gly His Gly Ile
100 105 110

Glu Phe Ala Pro Met Tyr Lys Ile Asn Tyr Ser Arg Asp Gly Thr Arg
115 120 125

Trp Ile Ser Trp Arg Asn Arg His Gly Lys Gln Val Leu Asp Gly Asn

130	135	140
Ser Asn Pro Tyr Asp Ile Phe Leu Lys Asp Leu Glu Pro Pro Ile Val		
145	150	155 160
Ala Arg Phe Val Arg Phe Ile Pro Val Thr Asp His Ser Met Asn Val		
	165	170 175
Cys Met Arg Val Glu Leu Tyr Gly Cys Val Trp Leu Asp Gly Leu Val		
	180	185 190
Ser Tyr Asn Ala Pro Ala Gly Gln Gln Phe Val Leu Pro Gly Gly Ser		
	195	200 205
Ile Ile Tyr Leu Asn Asp Ser Val Tyr Asp Gly Ala Val Gly Tyr Ser		
	210	215 220
Met Thr Glu Gly Leu Gly Gln Leu Thr Asp Gly Val Ser Gly Leu Asp		
225	230	235 240
Asp Phe Thr Gln Thr His Glu Tyr His Val Trp Pro Gly Tyr Asp Tyr		
	245	250 255
Val Gly Trp Arg Asn Glu Ser Ala Thr Asn Gly Tyr Ile Glu Ile Met		
	260	265 270
Phe Glu Phe Asp Arg Ile Arg Asn Phe Thr Thr Met Lys Val His Cys		
	275	280 285
Asn Asn Met Phe Ala Lys Gly Val Lys Ile Phe Lys Glu Val Gln Cys		
	290	295 300
Tyr Phe Arg Ser Glu Ala Ser Glu Trp Glu Pro Asn Ala Ile Ser Phe		
305	310	315 320
Pro Leu Val Leu Asp Asp Val Asn Pro Ser Ala Arg Phe Val Thr Val		
	325	330 335
Pro Leu His His Arg Met Ala Ser Ala Ile Lys Cys Gln Tyr His Phe		
	340	345 350
Ala Asp Thr Trp Met Met Phe Ser Glu Ile Thr Phe Gln Ser Asp Ala		
	355	360 365
Ala Met Tyr Asn Asn Ser Glu Ala Leu Pro Thr Ser Pro Met Ala Pro		
	370	375 380
Thr Thr Tyr Asp Pro Met Leu Lys Val Asp Asp Ser Asn Thr Arg Ile		
385	390	395 400
Leu Ile Gly Cys Leu Val Ala Ile Ile Phe Ile Leu Leu Ala Ile Ile		
	405	410 415
Val Ile Ile Leu Trp Arg Gln Phe Trp Gln Lys Met Leu Glu Lys Ala		
	420	425 430
Ser Arg Arg Met Leu Asp Asp Glu Met Thr Val Ser Leu Ser Leu Pro		

435					440					445						
Ser	Asp	Ser	Ser	Met	Phe	Asn	Asn	Asn	Arg	Ser	Ser	Ser	Pro	Ser	Glu	
450					455					460						
Gln	Gly	Ser	Asn	Ser	Thr	Tyr	Asp	Arg	Ile	Phe	Pro	Leu	Arg	Pro	Asp	
465					470					475					480	
Tyr	Gln	Glu	Pro	Ser	Arg	Leu	Ile	Arg	Lys	Leu	Pro	Glu	Phe	Ala	Pro	
485					490					495						
Gly	Glu	Glu	Glu	Ser	Gly	Cys	Ser	Gly	Val	Val	Lys	Pro	Val	Gln	Pro	
500					505					510						
Ser	Gly	Pro	Glu	Gly	Val	Pro	His	Tyr	Ala	Glu	Ala	Asp	Ile	Val	Asn	
515					520					525						
Leu	Gln	Gly	Val	Thr	Gly	Gly	Asn	Thr	Tyr	Ser	Val	Pro	Ala	Val	Thr	
530					535					540						
Met	Asp	Leu	Leu	Ser	Gly	Lys	Asp	Val	Ala	Val	Glu	Glu	Phe	Pro	Arg	
545					550					555					560	
Lys	Leu	Leu	Thr	Phe	Lys	Glu	Lys	Leu	Gly	Glu	Gly	Gln	Phe	Gly	Glu	
565					570					575						
Val	His	Leu	Cys	Glu	Val	Glu	Gly	Met	Glu	Lys	Phe	Lys	Asp	Lys	Asp	
580					585					590						
Phe	Ala	Leu	Asp	Val	Ser	Ala	Asn	Gln	Pro	Val	Leu	Val	Ala	Val	Lys	
595					600					605						
Met	Leu	Arg	Ala	Asp	Ala	Asn	Lys	Asn	Ala	Arg	Asn	Asp	Phe	Leu	Lys	
610					615					620						
Glu	Ile	Lys	Ile	Met	Ser	Arg	Leu	Lys	Asp	Pro	Asn	Ile	Ile	His	Leu	
625					630					635					640	
Leu	Ser	Val	Cys	Ile	Thr	Asp	Asp	Pro	Leu	Cys	Met	Ile	Thr	Glu	Tyr	
645					650					655						
Met	Glu	Asn	Gly	Asp	Leu	Asn	Gln	Phe	Leu	Ser	Arg	His	Glu	Pro	Pro	
660					665					670						
Asn	Ser	Ser	Ser	Ser	Asp	Val	Arg	Thr	Val	Ser	Tyr	Thr	Asn	Leu	Lys	
675					680					685						
Phe	Met	Ala	Thr	Gln	Ile	Ala	Ser	Gly	Met	Lys	Tyr	Leu	Ser	Ser	Leu	
690					695					700						
Asn	Phe	Val	His	Arg	Asp	Leu	Ala	Thr	Arg	Asn	Cys	Leu	Val	Gly	Lys	
705					710					715					720	
Asn	Tyr	Thr	Ile	Lys	Ile	Ala	Asp	Phe	Gly	Met	Ser	Arg	Asn	Leu	Tyr	
725					730					735						
Ser	Gly	Asp	Tyr	Tyr	Arg	Ile	Gln	Gly	Arg	Ala	Val	Leu	Pro	Ile	Arg	

740	745	750
Trp Met Ser Trp Glu Ser Ile Leu Leu Gly Lys Phe Thr Thr Ala Ser		
755	760	765
Asp Val Trp Ala Phe Gly Val Thr Leu Trp Glu Thr Phe Thr Phe Cys		
770	775	780
Gln Glu Gln Pro Tyr Ser Gln Leu Ser Asp Glu Gln Val Ile Glu Asn		
785	790	795
Thr Gly Glu Phe Phe Arg Asp Gln Gly Arg Gln Thr Tyr Leu Pro Gln		
	805	810
		815
Pro Ala Ile Cys Pro Asp Ser Val Tyr Lys Leu Met Leu Ser Cys Trp		
	820	825
		830
Arg Arg Asp Thr Lys Asn Arg Pro Ser Phe Gln Glu Ile His Leu Leu		
	835	840
		845
Leu Leu Gln Gln Gly Asp Glu		
850	855	

<210> 2

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Human DDR2 protein transmembrane domain synthetic construct (400~420)

<400> 2

Ile Leu Ile Gly Cys Leu Val Ala Ile Ile Phe Ile Leu Leu Ala Ile
1 5 10 15

Ile Val Ile Ile Leu Trp
20

<210> 3

<211> 415

<212> PRT

<213> Artificial Sequence

<220>

<223> Human DDR2 protein C-terminal tyrosine kinase active domain synthetic construct (441~855)

<400> 3

Met Thr Val Ser Leu Ser Leu Pro Ser Asp Ser Ser Met Phe Asn Asn
1 5 10 15

Asn Arg Ser Ser Ser Pro Ser Glu Gln Gly Ser Asn Ser Thr Tyr Asp

20	25	30
Arg Ile Phe Pro Leu Arg Pro Asp Tyr Gln Glu Pro Ser Arg Leu Ile		
35	40	45
Arg Lys Leu Pro Glu Phe Ala Pro Gly Glu Glu Glu Ser Gly Cys Ser		
50	55	60
Gly Val Val Lys Pro Val Gln Pro Ser Gly Pro Glu Gly Val Pro His		
65	70	75
Tyr Ala Glu Ala Asp Ile Val Asn Leu Gln Gly Val Thr Gly Gly Asn		
85	90	95
Thr Tyr Ser Val Pro Ala Val Thr Met Asp Leu Leu Ser Gly Lys Asp		
100	105	110
Val Ala Val Glu Glu Phe Pro Arg Lys Leu Leu Thr Phe Lys Glu Lys		
115	120	125
Leu Gly Glu Gly Gln Phe Gly Glu Val His Leu Cys Glu Val Glu Gly		
130	135	140
Met Glu Lys Phe Lys Asp Lys Asp Phe Ala Leu Asp Val Ser Ala Asn		
145	150	155
Gln Pro Val Leu Val Ala Val Lys Met Leu Arg Ala Asp Ala Asn Lys		
165	170	175
Asn Ala Arg Asn Asp Phe Leu Lys Glu Ile Lys Ile Met Ser Arg Leu		
180	185	190
Lys Asp Pro Asn Ile Ile His Leu Leu Ser Val Cys Ile Thr Asp Asp		
195	200	205
Pro Leu Cys Met Ile Thr Glu Tyr Met Glu Asn Gly Asp Leu Asn Gln		
210	215	220
Phe Leu Ser Arg His Glu Pro Pro Asn Ser Ser Ser Ser Asp Val Arg		
225	230	235
Thr Val Ser Tyr Thr Asn Leu Lys Phe Met Ala Thr Gln Ile Ala Ser		
245	250	255
Gly Met Lys Tyr Leu Ser Ser Leu Asn Phe Val His Arg Asp Leu Ala		
260	265	270
Thr Arg Asn Cys Leu Val Gly Lys Asn Tyr Thr Ile Lys Ile Ala Asp		
275	280	285
Phe Gly Met Ser Arg Asn Leu Tyr Ser Gly Asp Tyr Tyr Arg Ile Gln		
290	295	300
Gly Arg Ala Val Leu Pro Ile Arg Trp Met Ser Trp Glu Ser Ile Leu		
305	310	315
Leu Gly Lys Phe Thr Thr Ala Ser Asp Val Trp Ala Phe Gly Val Thr		

325	330	335
Leu Trp Glu Thr Phe Thr Phe Cys Gln Glu Gln Pro Tyr Ser Gln Leu		
340	345	350
Ser Asp Glu Gln Val Ile Glu Asn Thr Gly Glu Phe Phe Arg Asp Gln		
355	360	365
Gly Arg Gln Thr Tyr Leu Pro Gln Pro Ala Ile Cys Pro Asp Ser Val		
370	375	380
Tyr Lys Leu Met Leu Ser Cys Trp Arg Arg Asp Thr Lys Asn Arg Pro		
385	390	395
		400
Ser Phe Gln Glu Ile His Leu Leu Leu Leu Gln Gln Gly Asp Glu		
405	410	415

<210> 4
 <211> 1608
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Full-length src c-DNA synthetic construct

<400> 4	
atgggcagca acaagagcaa gccaaggac gccagccagc ggcgccgcag cctggagccc	60
tcggaaaacg tgcacggggc agggggcgcc ttcccggcct cacagacacc gagcaagccc	120
gcctccgccg acggccaccg cgggcccagc gccgccttcg tgccgcccgc ggccgagccc	180
aagctcttcg gaggttcaa ctctcggac accgtcacct ccccgagag ggcgggggct	240
ctggcaggtg gggtgaccac ctttgtggcc ctctatgact atgagtcacg gacagagact	300
gacctgtcct tcaagaaagg ggagcggctg cagattgtta acaacacgga gggagactgg	360
tggctggcac actcgtgag cacgggacag accggttaca tcccagcaa ctatgtggcg	420
ccctccgact ccatccaggc tgaggagtgg tactttggta agatcactag acgagaatca	480
gagcggctgc tgctcaacgc cgagaacccg agagggacct tcctcgtgag ggagagtgag	540
accacaaaag gtgcctactg cctctctgta tccgacttcg acaatgccaa gggctctaaat	600
gtgaaacact acaagatccg caagctggac agcggcggtt tctacatcac ctcccgcacc	660
cagttcaaca gcctgcagca gctcgtggct tactactcca aacatgctga tggcctgtgt	720
caccgcctca ctaccgtatg tcccacatcc aagcctcaga ccagggatt ggccaaggat	780
gcgtgggaga tccccggga gtccctgcgg ctggaggtca agctgggcca gggttgcttc	840
ggagaggtgt ggatggggac ctggaacggc accacgaggg ttgccatcaa aactctgaag	900

ccaggcacca tgtccccaga ggccttcctg caggaggccc aagtcatgaa gaaactgagg	960
cacgagaaac tgggtgcagct gtatgctgtg gtgtcggaag aaccatttta cattgtgaca	1020
gagtacatga acaaggggag tctgctggac tttctcaagg gggaaacggg caaatatttg	1080
cggctacccc agctggtgga catgtctgct cagatcgctt caggcatggc ctatgtggag	1140
cggatgaact atgtgcaccg ggaccttcga gccgccaata tcctagtagg ggagaacctg	1200
gtgtgcaaag tggccgactt tgggttggcc cggctcatag aagacaacga atacacagcc	1260
cggcaaggtg ccaaattccc catcaagtgg accgcccctg aagctgctct gtacggcagg	1320
ttcaccatca agtcggatgt gtggtccttt gggattctgc tgaccgagct caccactaag	1380
ggaagagtgc cctatcctgg gatggtgaac cgtgaggttc tggaccaggt ggagcggggc	1440
taccggatgc cttgtccccc cgagtgcctc gagtccctgc atgaccttat gtgccagtgc	1500
tggcggaagg agcccgagga gcggcccacc ttcgagtacc tgcaggcctt cctggaagac	1560
tactttacgt ccactgagcc acagtaccag cccggggaga acctatag	1608

<210> 5
 <211> 1449
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Full-length fyn gene synthetic construct

<400> 5	
atgggctgtg tgcaatgtaa ggataaagaa gcaacaaaac tgacggagga gagggacggc	60
agcctgaacc agagctctgg gtaccgctat ggcacagacc ccacccctca gcactacccc	120
agcttcggtg tgacctccat ccccaactac aacaacttcc acgcagccgg gggccaagga	180
ctcaccgtct ttggaggtgt gaactcttcg tctcatacgg ggaccttgcg tacgagagga	240
ggaacaggag tgacactctt tgtggccctt tatgactatg aagcacggac agaagatgac	300
ctgagttttc acaaaggaga aaaatttcaa atattgaaca gctcggagg agattggtgg	360
gaagcccgt ccttgacaac tggagagaca ggttacattc ccagcaatta tgtggctcca	420
gttgactcta tccaggcaga agagtggtag tttggaaaac ttggccgaaa agatgctgag	480
cgacagctat tgtcctttgg aaacccaaga ggtacctttc ttatccgcga gagtgaaacc	540
accaaaggtg cctattcact ttctatccgt gattgggatg atatgaaagg agaccatgtc	600
aaacattata aaattcgcaa acttgacaat ggtggatact acattaccac ccgggccag	660

tttgaaacac ttcagcagct tgtacaacat tactcaggta cctggaatgg aaacacaaaa	720
gtagccataa agactcttaa accaggcaca atgtcccccg aatcattcct tgaggaagcg	780
cagatcatga agaagctgaa gcacgacaag ctggtccagc tctatgcagt ggtgtctgag	840
gagcccatct acatcgtcac cgagtatatg aacaaaggaa gtttactgga tttcttaaaa	900
gatggagaag gaagagctct gaaattacca aatcttgtgg acatggcagc acaggtggct	960
gcaggaatgg cttacatcga gcgcatgaat tatatccata gagatctgcg atcagcaaac	1020
attctagtgg ggaatggact catatgcaag attgctgact tcggattggc ccgattgata	1080
gaagacaatg agtacacagc aagacaaggt gcaaagttcc ccatcaagtg gacggcccc	1140
gaggcagccc tgtacgggag gttcacaatc aagtctgacg tgtggtcttt tggaatctta	1200
ctcacagagc tggtcaccaa aggaagagtg ccatacccag gcatgaacaa ccgggaggtg	1260
ctggagcagg tggagcgagg ctacaggatg ccctgccgcg aggactgcc catctctctg	1320
catgagctca tgateccactg ctggaaaaag gaccctgaag aacgccccac ttttgagtac	1380
ttgcagagct tcctggaaga ctactttacc gcgacagagc ccagtacca acctggtgaa	1440
aacctgtaa	1449

<210> 6
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> 5' primer for PCR of DDR2 protein

<400> 6	
cccggatcca tgacagtcag cctttccct	29

<210> 7
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> 3' primer for PCR of DDR2 protein

<400> 7	
gggtctagat cactcgtcgc cttgttgaag	30

<210> 8

<211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> 5' primer for PCR of human full-length src c-DNA

 <400> 8
 ggggggattcg acggatcggg agatctcccg 30

 <210> 9
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> 3' primer for PCR of human full-length src c-DNA

 <400> 9
 cccgaattcg acgtcaggtg gcacttttcg ggg 33

 <210> 10
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Forward primer containing Nco I site for mutation of K608A

 <400> 10
 gccgtcacca tggacctg 18

 <210> 11
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Reverse primer containing Bam HI site for mutation of K608A

 <400> 11
 gcccgccct ggatccgg 18

 <210> 12
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Forward primer containing K608A mutation

<400> 12

gtggctgtgg caatgctccg a

21

<210> 13

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Reverse primer containing K608A mutation

<400> 13

tcggagcatt gccacagcca c

21

<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' primer containing Nco I site for tyrosine mutation

<400> 14

actcagtgcc tgccgtcacc

20

<210> 15

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' primer for mutation of Y740F

<400> 15

cccggccctg gatccggtaa tagtcaccac tgaacagggtt c